

SEQUENCE LISTING

<110> Hope, Ralph Graham
McLauchlan, John

<120> VIRAL THERAPEUTICS

<130> DY0U17.001CP1

<150> US 09/201,916

<151> 1998-12-01

<150> GB 9825951.8

<151> 1998-11-26

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 630

<212> DNA

<213> Hepatitis C Virus

<220>

<221> CDS

<222> (43)...(630)

<400> 1

gggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca cc atg agc acg aat 54
Met Ser Thr Asn
1

cct aaa cct caa aga aaa acc aaa cgt aac acc aac cgt cgc cca cag 102
Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln
5 10 15 20

gac gtt aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt tac ttg 150
Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu
25 30 35

ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg acg agg aag act 198
Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr
40 45 50

tcc gag cgg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gca 246
Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala
55 60 65

cgt cgg ccc aag ggc agg aac tgg gct cag ccc ggg tat cct tgg ccc 294
Arg Arg Pro Lys Gly Arg Asn Trp Ala Gln Pro Gly Tyr Pro Trp Pro
70 75 80

ctc tat ggc aat gag ggt tgc ggg tgg gcg gga tgg ctc ctg tcc ccc 342
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro
 85 90 95 100

agt ggc tct cgg cct agt tgg ggc ccc aac gac ccc cga cgt agg tcg 390
 Ser Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro Arg Arg Arg Ser
 105 110 115

cgc aat ttg ggt aag gtc atc gat acc ctt acg tgc ggc ttc gtc gat 438
 Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Val Asp
 120 125 130

ctc atg ggg tac ata ccg ctc gtc ggc gcc cct ctt aga ggc gct gcc 486
 Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Arg Gly Ala Ala
 135 140 145

agg gcc ctg gcg cat ggc gtc cgg gtt ctg gaa gac ggt gtg aac tat 534
 Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr
 150 155 160

gca aca ggt aac ctt cct ggt tgc tct ttc tct atc ttc ctt ctg gcc 582
 Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala
 165 170 175 180

ctg ctc tct tgc ctg act gtg ccc gct tca gcc tac caa gtg cgc aac 630
 Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
 185 190 195

<210> 2

<211> 60

<212> DNA

<213> Hepatitis C Virus

<220>

<221> CDS

<222> (1)...(60)

<223> Corresponds to aa 125 to 144 of SEQ ID. No. 1

<400> 2

acc ctt acg tgc ggc ttc gtc gat ctc atg ggg tac ata ccg ctc gtc 48
 Thr Leu Thr Cys Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val
 1 5 10 15

ggc gcc cct ctt 60
 Gly Ala Pro Leu
 20

<210> 3

<211> 18

<212> DNA

<213> Hepatitis C Virus

<220>
 <221> CDS
 <222> (1)...(18)
 <223> Corresponds to aa 161-166 of SEQ ID. No. 1

<400> 3
 ggt gtg aac tat gca aca
 Gly Val Asn Tyr Ala Thr
 1 5

18

<210> 4
 <211> 1900
 <212> DNA
 <213> Human

<220>
 <221> misc_feature
 <222> (1)...(1900)
 <223> n = A,T,C or G

<400> 4
 cgtcttcggg acgcgcccgc tcttcgcctt tcgctgcagt ccgtcgattt ctttctccag 60
 gaagaaaaat ggcattccgtt gcagttgatc cacaaccgag tgtggtgact cgggtggtca 120
 acctgccctt ggtgagctcc acgtatgacc tcatgtcctc agcctatctc agtacaaagg 180
 accagtatcc ctacctgaag tctgtgtgtg agatgscaga gaacggtgtg aagaccatca 240
 cctccgtggc catgaccagt gctctgccca tcatccagaa gctagagccg caaattgcag 300
 ttgccgatac ctatgcctgt aaggggctag acaggattga ggagagactg cctattctga 360
 atcagccatc aactcagatt gttgccaatg ccaaaggcgc tgtgactggg gcaaaagatg 420
 ctgtgacgac tactgtgact ggggccaaagg attctgtngc cagcacgatc acaggggtga 480
 tggacaagac caaaggggca gtgactggca gtgtggagaa gaccaagtct gtggtcagtg 540
 gcagcattaa cacagtcttg gggagtcgga tgatgcagct cgtgagcagt ggcgtagaaa 600
 atgcactcac caaatcagag ctgttggtag aacagtacct ccctctcact gaggaagaac 660
 tagaaaaaga agcaaaaaaa gttgaaggat ttgatctggt tcagaagcca agttattatg 720
 ttagactggg atccctgtct accaagcttc actcccgctg ctaccagcag gctctcagca 780
 ggggttaaaga agctaagcaa aaaagccaac agaccatttc tcagctccat tctactgttc 840
 acctgattga atttgccagg aagaatgtgt atagtgccaa tcagaaaatt caggatgctc 900
 aggataagct ctacctctca tgggtagagt ggaaaaggag cattggatat gatgatactg 960
 atgagtccca ctgtgctgag cacattgagt cacgtactct tgcaattgcc cgcaacctga 1020
 ctacgcagct ccagaccacg tgccacaccc tcctgtccaa catccaaggt gtaccacaga 1080
 acatccaaga tcaagccaag cacatggggg tgatggcagg cgacatctac tcagtgttcc 1140
 gcaatgctgc ctccctttaa gaagtgtctg acagcctcct cacttctagc aaggggcagc 1200
 tgcagaaaat gaaggaatct ttagatgacg tgatggatta tcttgttaac aacacgcccc 1260
 tcaactggct ggtaggtccc ttttatcctc agctgactga gtctcagaat gctcaggacc 1320
 aaggtgcaga gatggacaag agcagccagg agaccagcg atctgagcat aaaactcatt 1380
 aaacctgccc ctatcactag tgcatgctgt ggccagacag atgacacctt ttgttatgtt 1440
 gaaattaact tgctaggcaa ccctaaattg ggaagcaagt agctagtata aaggccctca 1500
 attgtagttg tttccagctg aattaagagc tttaaagttt ctggcattag cagatgattt 1560
 ctgttcacct ggtaagaaaa gaatgatagg cttgtcagag cctatagcca gaactcagaa 1620
 aaaattcaaa tgcacttatg ttctcattct atggccattg tggtgcctct gttactgttt 1680
 gtattgaata aaaacatctt catgtgggct ggggtagaaa ctggtgtctg ctctgggtgtg 1740
 atctgaaaag gcgtcttcac tgcttttatct catgatgctt gcttgtaaaa cttgatttta 1800
 gtttttcatt tctcaaatag gaatactacc tttgaattca ataaaattca ctgcaggata 1860
 gaccagttna gnagcaaaaca nncangtaca cnnaaganac 1900

<210> 5
 <211> 437
 <212> PRT
 <213> Human

<220>
 <221> VARIANT
 <222> (1)...(437)
 <223> Xaa = Any Amino Acid

<400> 5
 Met Ala Ser Val Ala Val Asp Pro Gln Pro Ser Val Val Thr Arg Val
 1 5 10 15
 Val Asn Leu Pro Leu Val Ser Ser Thr Tyr Asp Leu Met Ser Ser Ala
 20 25 30
 Tyr Leu Ser Thr Lys Asp Gln Tyr Pro Tyr Leu Lys Ser Val Cys Glu
 35 40 45
 Met Xaa Glu Asn Gly Val Lys Thr Ile Thr Ser Val Ala Met Thr Ser
 50 55 60
 Ala Leu Pro Ile Ile Gln Lys Leu Glu Pro Gln Ile Ala Val Ala Asp
 65 70 75 80
 Thr Tyr Ala Cys Lys Gly Leu Asp Arg Ile Glu Glu Arg Leu Pro Ile
 85 90 95
 Leu Asn Gln Pro Ser Thr Gln Ile Val Ala Asn Ala Lys Gly Ala Val
 100 105 110
 Thr Gly Ala Lys Asp Ala Val Thr Thr Thr Val Thr Gly Ala Lys Asp
 115 120 125
 Ser Val Ala Ser Thr Ile Thr Gly Val Met Asp Lys Thr Lys Gly Ala
 130 135 140
 Val Thr Gly Ser Val Glu Lys Thr Lys Ser Val Val Ser Gly Ser Ile
 145 150 155 160
 Asn Thr Val Leu Gly Ser Arg Met Met Gln Leu Val Ser Ser Gly Val
 165 170 175
 Glu Asn Ala Leu Thr Lys Ser Glu Leu Leu Val Glu Gln Tyr Leu Pro
 180 185 190
 Leu Thr Glu Glu Glu Leu Glu Lys Glu Ala Lys Lys Val Glu Gly Phe
 195 200 205
 Asp Leu Val Gln Lys Pro Ser Tyr Tyr Val Arg Leu Gly Ser Leu Ser
 210 215 220
 Thr Lys Leu His Ser Arg Ala Tyr Gln Gln Ala Leu Ser Arg Val Lys
 225 230 235 240
 Glu Ala Lys Gln Lys Ser Gln Gln Thr Ile Ser Gln Leu His Ser Thr
 245 250 255
 Val His Leu Ile Glu Phe Ala Arg Lys Asn Val Tyr Ser Ala Asn Gln
 260 265 270
 Lys Ile Gln Asp Ala Gln Asp Lys Leu Tyr Leu Ser Trp Val Glu Trp
 275 280 285
 Lys Arg Ser Ile Gly Tyr Asp Asp Thr Asp Glu Ser His Cys Ala Glu
 290 295 300
 His Ile Glu Ser Arg Thr Leu Ala Ile Ala Arg Asn Leu Thr Gln Gln
 305 310 315 320
 Leu Gln Thr Thr Cys His Thr Leu Leu Ser Asn Ile Gln Gly Val Pro
 325 330 335
 Gln Asn Ile Gln Asp Gln Ala Lys His Met Gly Val Met Ala Gly Asp
 340 345 350

Ile Tyr Ser Val Phe Arg Asn Ala Ala Ser Phe Lys Glu Val Ser Asp
355 360 365
Ser Leu Leu Thr Ser Ser Lys Gly Gln Leu Gln Lys Met Lys Glu Ser
370 375 380
Leu Asp Asp Val Met Asp Tyr Leu Val Asn Asn Thr Pro Leu Asn Trp
385 390 395 400
Leu Val Gly Pro Phe Tyr Pro Gln Leu Thr Glu Ser Gln Asn Ala Gln
405 410 415
Asp Gln Gly Ala Glu Met Asp Lys Ser Ser Gln Glu Thr Gln Arg Ser
420 425 430
Glu His Lys Thr His
435

<210> 6
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> branched peptide containing residues 5-27 of HCV
core protein

<221> VARIANT
<222> (1)...(31)
<223> Xaa = Ala or Pro at position 1, and Ile or Asn at
position 12

<400> 6
Xaa Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Xaa Arg Arg Pro Gln
1 5 10 15
Asp Val Lys Phe Pro Gly Gly Lys Lys Lys Lys Lys Lys Ala
20 25 30

<210> 7
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 7
gctgagatct a

11

<210> 8
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 8
gtaaccttcc tggttgctct tgagatcta 29

<210> 9
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 9
gtaacctttg agatcta 17

<210> 10
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 10
ctggcgcatg gagatcta 18

<210> 11
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 11
ctggcccatg gtgttaacta tgcaacag 28

<210> 12
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 12
ctggcccatg gcgtccgggt tctggaagac g 31

<210> 13
<211> 37
<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotides used to construct HCV core
protein deletion plasmids

<400> 13

cgatagagggc gctgccaggg ccctggcggtg agatcta

37

<210> 14

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> HCV1 oligonucleotide for plasmid construction

<400> 14

catgggggtac atagcgctcg tcggcgccgc cttagagggc gctgcgaggg cc

52

<210> 15

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> HCV2 oligonucleotide for plasmid construction

<400> 15

ctagagagcg caagacgccc cgcgtcaccg gcggcg

36

<210> 16

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> primer derived from GBV-B, nucleotides 428-448,
for plasmid construction

<400> 16

ggagatctcg tagaccgtag cacatg

26

<210> 17

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer derived from GBV-B, nucleotides 842-868,
for plasmid construction

<400> 17

ggggatccct agtggacacc gaaccaacca gtagccca

38

<210> 18
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> primer derived from GBV-B, nucleotides 1003-1029,
for plasmid construction

<400> 18
ggggatcctc agatcacaca accaggtcgc tgtagg

36

<210> 19
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> primer derived from GBV-B, nucleotides 1618-1639,
for plasmid construction

<400> 19
gggtactcta gaggatagg cctgggc

27

<210> 20
<211> 49
<212> DNA
<213> Artificial Sequence

<220>

<223> primer derived from GBV-B for plasmid construction

<400> 20
ctagagagcg caagacgccg cgggtcaccg gtggctctcg caatcttgg

49